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Scoring table:
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Perfect score:
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seq length: 2000000000
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1098
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is the number of results predicted by chance to have
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match 168136 183485 209718 185834 185834 19087 203131 203982 207040 209836 210736 189464 195909 150438 165965 167122 168216 173445 174617 42740 110394 129109 135862 147874 6782 179514 Length 264864 15121 15649 39403 DВ 10 AC091099 AC009632 AC009632 AX345694 AX345679 AC135128 AR290313 AX114392 AX281468 AX348804 AX345350 AX345350 AX344831 AX345350 AX345350 AX34633 AC090706 AX365332 AC091217 AC012217 AC012287 AC012287 AC012287 AC012287 AC0123138 AC0718876 AC105180 AC115180 AC115180 AC115180 AC115180 AC115180 BD196412 BD196564 AC100813 AC067854 AC091984 AC091926 AC092792 BX649211 ij AC13444 AC100813 Homo sapi AF287957 Homo sapi AC022878 Homo sapi AC091099 Homo sapi AC0910932 Homo sapi AC009632 Homo sapi AC009632 Homo sapi AX345679 Sequence AX345679 Sequence AX315128 Rattus muscu AC135128 Rattus muscu AC135128 Rattus muscu AC135128 Sequence AX14392 Sequence AX346581 Sequence AX346581 Sequence AX345810 Sequence AX345810 Sequence AX344831 Sequence AX344831 Sequence AX344831 Sequence AX344831 Sequence AX344831 Sequence AX348975 Sequence AX348975 Sequence AC090706 Homo sapi AC030386 Homo sapi AL390239 Human DNA AC025757 Homo sapi AC01278 Homo sapi AC012287 Homo sapi AC012287 Homo sapi AC013398 Homo sapi AC013398 Homo sapi AC013398 Homo sapi AC016180 Homo sapi AC105180 Homo sapi AC105184 Homo sapi AC105184 Homo sapi AC09194 Homo sapi AC091954 Homo sapi AC091954 Homo sapi AC09196 Homo sapi AC091970 Homo sapi AC091971 Homo sapi AC091971 Homo sapi AC091972 Homo sapi AC091972 Homo sapi AC091973 Rattus no AE014841 Plasmodiu BD196412 Prostatic BD196564 Prostatic Description

TITLE JOURNAL	REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 BD196412
Prostatic cancer gene Patent: JP 2002516657-A 1 11-JUN-2002;	<pre>1 (bases 1 to 56516) Cohen,D., Blumenfeld,M., Chumakov,I. and Bouqueleret,L.</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	JP 2002516657-A/1.	BD196412.1 GI:33006182	BD196412	Prostatic cancer gene.	BD196412 56516 bp DNA linear PAT 17-JUL-2003	

ALIGNMENTS

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COMMENT
                                                                               FEATURES
source
       ORIGIN
                                                                                                           GENSET

OCEN Mono sepients (human)
BN 17 2002516657-A/1
BP 11-UND-2002
BP 2002516657-A/1
BP 12-UND-2002
BP 200251999 UP 200052562
BP 22-DEC-1999 US 06/996506,09-SEP-1998 US 60/099658 PT

PARLEL COHEN MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERER PC
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REFERENCE
AUTHORS
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rostatic cancer gene
Patent: JP 200251657-A 153 11-JUN-2002;

GENSET
OS Homo sapiens (human)
PN JP 2002516657-A/153
PD 11-JUN-2002
PF 22-DEC-17
                                                                                                                                              pc C12N15/00,C12N15/00

CC exon2

CC exon3

CC exon4

CC exon5

CC exon6

CC upstream amplification primer 5-63

CC downstream amplification primer 99-622

CC upstream amplification primer 99-621

CC upstream amplification primer 99-621

CC upstream amplification primer 99-611

CC upstream amplification primer 4-76

CC downstream amplification primer 4-76

CC downstream amplification primer 4-77

CC downstream amplification primer 4-71

CC downstream amplification primer 4-72

CC downstream amplification primer 4-72

CC downstream amplification primer 4-72

CC downstream amplification primer 4-73

CC downstream amplification primer 99-610

CC upstream amplification primer 99-609

CC upstream amplification primer 99-609
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PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN WARTA BLUMENFELD, ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
                                             CC upstream amplification primer 99-609, upstream amplification primer 4-90 CC downstream amplification primer 99-607 downstream amplification primer 99-607 CC upstream amplification primer 99-607,
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CC downstream ammlification primer 5-47
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CC downstream ammlification 59-217
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÷	GTTTCTTGTTCCTGCATTTTTATTTTTATTGTATGGAGGGGACAAATAATTATTTTCTGT 60	Query Match 100.0%; Score 1098; DB 6; Length 56520; Best Local Similarity 100.0%; Pred. No. 0; Matches 1098; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	primer_bind 52199.	primer_bind 51826.	primer_bind 51667.	primer bind 51593. primer bind 29734.	FT primer_bind 5118351202 FT primer_bind 5114651165 FT primer_bind 5147951496	primer_bind 50964. primer_bind 50774.	primer bind 50541. primer bind 50940.	primer_bind 50271. primer_bind 50172. primer_bind 50573	primer_bind 49331. primer_bind 49830.	primer_bind 48217. primer_bind 48902.	primer bind 46186.	primer bind 40629. primer bind 41058.	primer bind 40531. primer bind 40932.	primer bind 35182. primer bind 39591.	primer bind 34916. primer bind 34702.	primer_bind 34624.	primer bind 32862. primer bind 32823.	primer_bind 25657. primer_bind 26537.	primer_bind 23111. primer_bind 25098.	primer_bind 18699. primer_bind 19164. primer_bind 22589.	primer_bind 18008. primer_bind 18423.	primer bind 17304. primer bind 17814.	primer bind 15994.	primer_bind 13617. primer_bind 13547. primer_bind 13962	12915. 13317. 13216.	FT primer bind 1162211639 FT primer bind 1201812037 FT primer bind 1193011947 FT primer bind 1233911947
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Eukaryota; Metazoa; Chordata; Catarrhini; Hom
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 165799)
Birren,B., Nusbaum,C. and Lander,E.
Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                       Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17048183. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                 Center: Whitehead Institute/ MIT Center
Contact: sequence_submissions@genome.wi.mit.edu
                                                     Web site: http://www-seq.wi.mit.edu
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                   TTACACCTTTCAACTCTAGGTTTAAAAAATAAGTGGTTCACAGTAGTTCTTGCAGAAGAA
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Center project name: L21488
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1 (bases 1 to 168136)
Reichwald, K., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Menzel, U., Polley, A., Schilhabel, M.B., Taudien, S., Wen, G. and Rosenthal, A.
                                     Biotechnology, Beutenberstr. 11, 5 (bases 1 to 168136)
                                                                                                          Biotechnology, Beutenberstr. 4 (bases 1 to 168136)
Lagemann, D. and Platzer, M.
                                                                                                                                                         Submitted (23-AUG-2001) Genome Analysis, Institute of M Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745,
                                                                                                                                                                                                                          3 (bases 1 to 168136)
Reichwald, K. and Platzer, M.
                                                                                                                                                                                                                                                               Submitted (14-JUL-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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7 (bases I to 168136)
Lagemann,D. and Platzer,M.
Direct Submission
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Lagemann, D. and Platzer, M.
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Submitted (03-ARR-2002) Genome Analysis, Institution
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This clone is overlapped by GS1-24F4, GS1-24F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality levels above 40 are expected to have less 1 error in 10,000 bp.
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All manually edited bases have been reduced to quality
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Center project name: H351
Center clone name: CTD-2541M15
                                                     28243.
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28243. .28507
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                                                                                                                                                             note="overlapping clone, overlapping"
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/clone="CTD-2541M15"
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/note="single stranded/single
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/note="single stranded/single
90439. .90940
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18995. .39017
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12247. .112576
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   ATGATCTGTGCTTGGCAGGTAAACCTGCTTCCAACAATTTAGTTGGATTTTTCTTGGAT 116784
                                                                                                                  AGGAATAAATAGCTATCTTCAAACATAAGACCCAAAGGAAAAAGATTTATAGTGATGTTC 116304
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                                                                           TATTTTCTTTTACATAGAATTTTTAAGCTGAAGAGAAGTAGTAGTAGGTCCATGAGATTT
                                                                                                                                                                                        GACTCATTTCTGAAGGGAGTTTTAGTAATTTAAGAGGTTATAAGTTTTTAAATAAAAGGT 116544
                                                                                                                                                                                                                                                                                          TTTATCAGCTTTCGTTTGCAAGGCTAGTGATGATTCTCTTGTTCTGTATAAAGTATTGTT 116484
                                                                                                                                                                                                                                                                                                          TTTATCAGCTTTCGTTTGCAAGGCTAGTGATGATTGTTCTCTTTGTTCTGTATAAAGTATTGTT 420
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                                                            TATTTTCTTTTACATAGAATTTTTAAGCTGAAGAGGAAGTAGTAGTAGGTCCATGAGATTT
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163686. 163687
/note="low quality region"
165389. 165603
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150458. .150522
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145776. .145927
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142575. .142734
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141144. 141340
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                                                                                                                                                                                                                                                                                                           RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukingalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Crant, G., Hagos, B., Heaford, A., L., Karatas, A., Klein, J., Howland, J., Lebine, R., Liu, G., Liu, G., Locke, K., Howland, J., Lebine, R., Liu, G., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrin, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., Meldrin, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Peterson, K., Pierre, N., Peterson, C., Roy, A., Santos, R., Severy, P., Spencer, B., Stange Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zodv. M.
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1 (bases 1 to 183485)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiess, clone RP11-15C20
                                     All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                           Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 this sequence version replaced gi:12313816.
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                                                                                                                                                                                                                                                                                                 Zimmer, A. and Zody, M.
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Institute/ MIT Center
          for
          Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
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Center clone name: 15_C_20
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                                                                        43876.
                 /note="assembly_fragment'
67158. .126278
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14380: gap of
25807: contig
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2538:
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7391: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lib="RPCI-11 Human
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gap of
contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 100 bp in length ig of 2767 bp in length 100 bp in length of 100 bp in length ig of 2442 bp in length ig of 4247 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 1387 bp in length
100 bp
of 1051 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
of 11427 bp in length
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of 1886 bp in length
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960	TATTTCTTTAGAATAAGTAATAAGAATTTTATAAGCTTTTTTATATTTCACGTAATTTGA	Оу 901	
77058	TAGGTCCTTCCAGAATCTCTCATTGGTACTGAAACTCAAATGGGTACTTTCTTCACCATT	Db 76999	
900	TAGGTCCTTCCAGAATCTCTCATTGGTACTGAAACTCAAATGGGTACTTTCTTCACCATT	Оу 841	
840 76998	GATAGAGAAATATTTCAGTCAGTGCTGCTAAAATTGTTCCTTATAACTCGTTTATCCTTT	Qy 781 Db 76939	
780 76938	TCTGGGTAAATACCTTTTTCTTCCCCAGTTTCACTTTATTTTCATATGTATCTCTGA	Qy 721 Db 76879	
720	ATGATCTGTGCTTGGCAGGTAAACCTGCTTCCAACAAATTTAGTTGGATTTTTCTTGGAT	Qy 661 Db 76819	
660 76818	TATTTTCTTTTACATAGAATTTTTAAGCTGAAGAGAAGTAGTAGTAGGTCCATGAGATTT	Qy 601 Db 76759	
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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AUTHORS
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CE 2 (bases 1 to 209718)

Barna, N., Bastien, V., Boguslavky, L., Boukhgalter, B., Brown, A.,

Barna, N., Bastien, V., Boguslavky, L., Boukhgalter, B., Brown, A.,

Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M.,

Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K.,

Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,

Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K.,

Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K.,

MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,

McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L.,

Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,

Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,

Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,

Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,

Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,

Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, V.,

Viel, R., Vo, A., Wilson, B., W., X., Wyman, D., Ye, W.J., Young, G.,

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77239 AACTTAAGTTCTCGTGAT 77256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77059 TATTTCTTTAGAATAAGTAATAAGAATTTTATAAGCTTTTTTATATTTCACGTAATTTGA 77118
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HOMO sapiens chromosome 8 clone RP11-782N1 map 8, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
AC091099.3 GI:22122960
HTG; HTGS PHASEN. ....
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
                                                                                                                                                                                                                                                                                                                                                            Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 209718)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavkty, L., Boukhigalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 209718)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-782N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIGITACTITCCIGIGCIGCCAAAACAGATCACCICAAACTAAGCGGCTTAAAATAATAG 77238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (human)
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FEATURES
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                 misc_feature
                                                misc_feature
                                                                                                                 misc_feature
                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:15290844. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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' be preserved.
'7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 (Consensus quality: 206063 bases at least Q40 (Consensus quality: 207712 bases at least Q20 (Consensus quality: 207712 bases at least Q20 (Consensus quality: 208309 bases at least Q20 (Consensus quality: 208309 bases at least Q20 (Consensus quality: 208309 bases; agarose-fp (Quality coverage: 8.8 in Q20 bases; sum-of-contigs Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: 782_N_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                104130
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208330
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80309
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74850. .76857
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'note="assembly_fragment'
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                                                                                                                                  clone_lib="RPCI-11 Human Male BAC"
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of 8569 bp in length
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,

Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Depayre, B., Devon, K., Dewar, K.,

Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,

Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,

Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L.,

Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,

Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,

Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,

Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Paylin, B.,

Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,

Tesfaye, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A.,

Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.

Direct Submission
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                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 185834)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-397K22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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185834 bp DNA 1
sapiens chromosome 8 clone RP11-397K22
ROGRESS ***, 48 unordered pieces.
                                                                                             site: http://www-seq.wi.mit.edu
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2 map 8, *** SEQUENCING
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NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
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g of 7172 bp in length
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f 100 bp
g of 2673 bp in 1
f 100 bp
g of 3940 bp in 1
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Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L.,
Karatas, A., Leboczky, J., Lieu, C., Locke, K., Macdonald, P.,
Marquis, N., McBwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 7, 2000 this sequence version replaced gi:5932606.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-397K22
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                                                                                                                                                                                                                                                                                                                                soon as it preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2099
Center clone name: 397_K_22
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                           site: http://www-seq.wi.mit.edu
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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33379. .35479
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/clone_lib="RPCI-11 Human Male BAC"
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23583. .25557
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12440. .13923
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/db_xref="taxon:32630"
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/db_xref="traxon:32630"
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Muzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blewald, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Duyan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-DEC-2003) Genome Sequencing Center, 4444 Fore Parkway, St. Louis, MO 63108, USA
On Dec 12, 2003 this sequence version replaced gi:23322797
                                                                                                                                                                                                                                                                                                                                                                               AC135128.2 GI:25138667
HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
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McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson,R.K.
The sequence of Mus musculus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: submissions@watson.wustl.edu
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Mammalia; Eutheria; Rodentia;
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/db_xref="taxon:10090"
/chromosome="18"
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REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

COMMENT

Center project name: Center clone name: CF Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Project Information

Center: Baylor Co Center code: BCM

College of Medicine

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Egan, A., Escotto, M., Eugene, C., Ewans, C.A., Falls, T., Pan, G., Ferrandez, S., Finley, M., Flaggy, M., Forbes, L., Foster, M., Gourax, M., Gabisi, A., Gatis, R., Garcia, A., Garrar, M., Gourax, M., Gabisi, A., Gatis, R., Garcia, A., Garrar, M., Gourax, M., Garrar, M., Marrar, M., Soderyrer, M., Soderyrer, M., Soderyrer, M., Soderyrer, M., Soderyrer, M., Soderyrer, M., Watsen, M., Walse, M., Tabor, M., Taror, M., Marrar, M., Watser, M., Walse, M., Tabor, M., Taror, M., Marrar, M., Watser, M., Walse, M., W
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                                                        1 (bases 1 to 47)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 1768 25-MAR-2003;
                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                     AR290033.1
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                                                                                                                                                                                                 Unknown.
                                                                                                                                                          Unclassified.
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261463. .263304
/note="wgs_end_extension
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/note="clone_boundary
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clone_end:Sp6"
4648._.5394
/note="clone_boundary
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/db_xref="taxon:10116"
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/organism="unknown"
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Sequence 61 from Patent W00129257.
AXI14392
                                                                                                                                                    Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with metastasis patent: WO 0177376-A 132 18-OCT-2001;
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                                                                                                                                                                                                                                                                    Sequence 132 from Patent AX281468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methods of genetic cluster analysis and use thereof Patent: WO 0129257-A 61 26-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schork, N. and Skierczynski, B.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 2.1%; Score 23; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Solarity 100.0%; I Conservative 0;
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/mol_type="unassigned DNA"
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                                                                                                                 Location/Qualifiers
1. .6070
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                note="chemically treated genomic DNA (Homo sapiens)"
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match 212007 224600 247570 12029 108277 110000 159453 187241 165799 168136 183485 209718 185834 Length DB AC009632 AX141275 AF37579 BAF37579 BC023550 BD196514 BD196514 BD196511 BD196518 BD196517 BD196517 BD196510 BD196520 BD196520 BD196520 BD196510 AC022578 AC091099 AC100813 AF287957 ij MX268078 BD196514 BD196514 BD196513 BD196513 BD196513 BD196513 BD196519 BD196520 BD196520 BD196520 BD196520 BD196530 BD196530 BD196530 BD196530 BD196530 BD196530 BD196531 BD1 AC009632 AX141275 Description Homo sapi Sequence Frostatic Prostatic Prostat Prostatic Prostatic Prostatic

TITLE JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	BD196412	RESULT 1
Prostatic cancer gene Patent: JP 2002516657-A 1 11-JUN-2002;	Cohen, D., Blumenfeld, M., Chumakov, I. and Bougueleret, L.	1 (bases 1 to 56516)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	JP 2002516657-A/1.	BD196412.1 GI:33006182	BD196412	Prostatic cancer gene.	BD196412 56516 bp DNA linear PAT 17-JUL-2003		

ALIGNMENTS

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OSS Homo segients (human)

PN 17-2002516657-A/1

PD 11-UND-2002

PF 20-DEC-1999 UP 200052562

PF 22-DEC-1999 UP 200052562

PF 22-DEC-1999 US 08/996506,09-SEP-1998 US 60/099658 PI

DANIEL COHEN MARTA BLUMENFELD,IIVA CHUMAKOV,LUDIE BODGELERRT PC
C12N15/09,C12N15/09,A01K87/027,C07K14/47,C07K16/68,G01N33/50 PC

C12N15/09,C12N15/09

PC C12N15/09,C12N15/00

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Location/Qualifiers
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GENACA GENERAL	Best Local Similarity 100.0%; Pred. No. 0; Matches 2324; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GTGGATCTGTGCACTGTTCGCAGGAAGAGAGGAGACAGAC
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Birren,B., Linton,L., Nusbaum,C., Boguslavkiy,L., Boukhgalter,B.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hilme,W., Iliev,I., Johnson,R.,
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HTG; HTGS PHASBI; HTGS FULLTOP; HTGS_CANCELLED.
HOmo sapiens (human)
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RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyn, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zimmer, A. and Zody, M.
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Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17048183.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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2728 62827: gap of 100 bp

8828 73470: contig of 10643 bp in length

4471 73570: gap of 100 bp

1571 81515: contig of 7945 bp in length

1516 81615: gap of 100 bp

1616 165799: contig of 84184 bp in length.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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Genome Sequencing Center Jena.
Direct Submission
Submitted (14-UUL-2000) Genome Ana
Biotechnology, Beutenberstr. 11, J
3 (bases 1 to 168136)
Reichwald, K. and Platzer, M.
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168136)
Reichwald, K., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Reichwald, Y., Polley, A., Schilhabel, M.B., Taudien, S., Wen, G. and Menzel, U., Polley, A., Schilhabel, M.B., Taudien, S., Wen, G. and
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Submitted (03-APR-2002) Genome Analysis, Institute of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one pUC18 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-JUL-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 7 (bases 1 to 168136) Lagemann, D. and Platzer, M. Direct Submission
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Lagemann, D. and Platzer, M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neighboring sequence information:
This clone is overlapped by GS1-24F4, GS1-24F4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Quality Assessment:
                                                                                                                                                                                                                                                                   Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                           This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                      Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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Center clone name: CTD-2541M15
Center clone name: CTD-2541M15
Center clone name: CTD-2541M15
Sequencing vector: pUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 16707 bases at least Q40
Consensus quality: 168133 bases at least Q30
Consensus quality: 168336 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
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                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                 chromosome="8"
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    DNA
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35987. .36115
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28243. .28507
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/clone="GS1-24F4"
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36073. .86097
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81070. .81071
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/8279. .78386
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Db 113302 ÁGÁGÁCTGCTGCGCÁGÁGÁGGGÁGÁGGCGGCGTCCCCCTTGCAAÁGGÁCTG 113361 QY 1198 GCAGTGAGCAGATGGGGACACTCGAGCTGCCCCGCGACCTGGGCCGAGCTGCCTACAACC 1257	Db 113242 GTGATGGGGAAAACACGGACCCTAATTCTGAAACACCCTGGTAGCGAGAACACGGCAGG 113301 Qy 1138 AGGGCTGCTGCGCACTCAGAGCGGAGGGGCTGAGGGGCGCGTCCCCTTGCAAAGGACTG 1197		OY 958 CACAGACTCTGAGGAAATGAAGGAAATGCTGAAAAGGTCTAATAAACAGTATG 1017 Db 113122 CAACAGACTCTGAGGAATGAAGCAAGGAATTCTGAAAAGGTCTAATAAACAGTATG 113181 OV 1018 GAAATATCCTTGAGGAATTGTTCTTCAGCTATGAAAAGGTCTAATTAACATTATC 1077	898 TACTITAATTACTACAGAAAAAAACGAGGCTCCTTATTAAAAAAAA	Qy 838 GTAGCTTTTAGTGAAGGCTACAAAAGTATGCTTTTTATGGATTACACATGTGCACGCAAC 897	Qy 778 GAAAGATCCAAAAGTCCTGTGGATCTGCTTTAACATCAATAAAACAGTTATCCACCCTTC 837	Qy 718 ACAACTATCCTTGAAAAGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGAGGA 777	558 ATATATATATATATATATATATATATATATATGGTAAAGCATTCGGCATTCTTTTAAAGT 71 	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	20 10	feature	sc_featur	sc_feature	80 B	- /note="single stranded/single chemistry sc_feature 117025117051 /note="single stranded/single chemistry sc_feature 118344118414	/note="single stranded/single chemistry 105600106813 /note="por product sequence only" 112247112576	chemistry
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114442 TCCGCTCCCCACAGCTGGCGAGGGTCACCCGGCCGGCCCGGCGGAC 114488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 this sequence version replaced gi:12313816. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L.,
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Homo sapiens clone RP11-15C20, WORKING DRAFT SEQUENCE, 11 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                   Insert size: 170000; agarose-fp
Insert size: 182485; sum-of-contigs
Quality coverage: 7.0 in Q20 bases; agarose-fp
Quality coverage: 6.5 in Q20 bas.
NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                         as soon as it is available and the accession number wil
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(bases 1 to 183485)
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                                                                                                                                                                                                                                                              Consensus quality: 179658 bases at least Q40 Consensus quality: 181356 bases at least Q30 Consensus quality: 182011 bases at least Q20 Tools and Tools 182011 bases at least Q20 Tools 182011 bases at least Q20 Tools 182011
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1387: contig of 1387 bp in length
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                                                                                                                                                                                      AGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGGAGGAAAGATCCAAAAGTC
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                                                                                                                                             CTGTGGATCTGCTTTAACATCAATAAAACAGTTATCCACCCTTCGTAGCTTTTAGTGAAG 853
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/db_xref="taxon: 9606"
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|mol_type="genomic DNA"
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126278: contig of 59121 bp
126378: gap of 100 bp
183485: contig of 57107 bp
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2053	1994 GAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCGT
1993 74252	1934 GCGACTGAGGCCCGGGAGCGGGGGGGGGGGGGGGGGGGG
1933	1874 TGGGAGCGGGTGGCGGCGGCGGCCGGGCCCGGGCGGTGATTGGCCGCCTGCTGGCC
1873 74132	1814 CCCGCACTCGCCTACCCGGCCCCGGGCGGCGGCGCGCCCATGCGGCTGGGGGCGGAGGC
1813 74072	1754 CCATCGATCCGGGAGGGCCGCGGGGTTCCCTTGCTTTGCCGCCGGGAGCGGCACGCAGC
1753 74012	1694 CCTGCCCCGGCAGGGGATGTGGCCATGGGTGAGGGTCATGGGGTGTGAGCATCCCTGAG
1693 73952	1634 CCGAGGTGGAACTATGGCAACGGGCGACCAATCAGAAGGCGCGTTGTTGCCGCGGAGCCCC
1633 73892	1574 CAGGTAGCTGTACTGCAACTGTCGGCCCAAACCAATCAAGAGACGTGTTATTGCCG 1
1573 73832	1514 CGCAGCCGGCCCAGCTGGGGAGCATGCGCAGTGGCCGGAGCCGGGTTGCCCGCGCCACAG 1
L513 73772	1454 TCCGGCCAGCACCCACCTTCACCCAGTTCCGTCAGTCGCCACCACCACCTCCCTTCCCGCGGC 1
L453	1394 AAACCTGACCGCGCGCACGTCCGGCCCGAGGGAGCAGAACAAGAGGCACCCCGGACCCTCC 1
1393	1334 CCCGGCGCCCAGGGGCTTGTGAGCAGCAGGTGCGCGTTCCAGGCAGCTCCAGCGACCCTT 1
1333 73592	1274 CAAGAATTAGACCTCCGATAACGTTAACACCCACTTTCTCACTGCTCTAATTGTGTGCAT 1
73532	1214 GACACTCGAGCTGCCCCGCGACCTGGGCCGAGCTGCCTACAACCTGGGCCCAGGTGCCTG 1
[213 73472	1154 TCAGAGCGGAGGCTGAGGAGGCGGCGTCCCCTTGCAAAGGACTGGCAGTGAGCAGATGGG 1
.153	1094 CGGACCCTAATTCTGAAACACCCTGGTAGCGAGAGAGACGGGCAGGAGGGGCTGCTGCGCAC 1
.093 73352	1034 ATTGTTCTCAGCTATGCATAAACATGTAATTATCATCATTACTGTGATGGGGAAAAACA 1
.033	974 AATGAAGCAAGAGTGAATTCTGAAAAGGTCTAATAAACAGTATGGAAATATCCTTGTGGG 1
3232	914 GAAAAAAACGAGGCTCCTTATTAAAAAAAAATCAGAAACAAGTCCAACAGACTCTGAGGA 9

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TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	RESULT 7 AC091099 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Оу 2; пь 74!	Qy 2: Db 74	Qy 2: Db 74	Qy 21 Db 74	Qy 20 Db 743	Db 742
Illev,I., Johnson,K., Johes,C., Karatas,A., Lakocque,K., Liamazares,R., Landers,T., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meddrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Myuyen,C., Norbu,C., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Sie,C., Rogov,P., Roman,J., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission Submitted (29-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkky,L., Boukhgalter,B., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,II., Johnson,R., Jones,C., Kamat,A.,	Mammalia, Eucheria, Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 209718) Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-782N1 Hipublished 2 (bases 1 to 209718) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Heaford, A., Horton, L., Hulme, W., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,	AC091099 AC091096 AC091099 AC091091 AC0910	2294 TGGCGAGGGTCACCCGGCCGGCCGGCCGAC 2324	2234 CCCGGGTCTCGGCGTCCACCCGAGCTCCCGGGGGGCGCGGACCTCTCCGCTCCCCCACAGC 2293	2174 GAGCATGGTGCTCTTCTTCCTCGAGAATTACACCGGGGTCCAGGTGAGCCGCCTCCCGCT 2233	2114 CGCCTTCCTGCCCGCCCCGCTTCTACCAAGCGCTGGACGACCGGCTGTACTGCGTCTACCA 2173	2054 CGTGCTCCTGGGCACCGACCTACGTGTTGGCCTGGGGGGTCTGGCGGCTGCTCTC 2113	74253 AAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCGT 74312

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FEATURES
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                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:15290844. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 206063 bases at least Q40 Consensus quality: 207712 bases at least Q20 Consensus quality: 207712 bases at least Q20 Consensus quality: 208309 bases at least Q20 Insert size: 205000; agarose-fp Insert size: 205000; agarose-fp Quality coverage: 8.8 in Q20 bases; agarose-fp Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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104230
120105
120205
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----- Project Information
Center project name: L12159
                                                                                                                                                                  152290
208330
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                           /mol_type="genomic un
/db_xref="taxon:9606"
/chromosome="8"
                                                                                        organism="Homo sapiens"
clone="RP11-782N1"
                                                                                                                               ocation/Qualifiers
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    Genome Center

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                                                                                        GACACTCGAGCTGCCCCGCGACCTGGGCCGAGCTGCCTACAACCTGGGCCCAGGTGCCTG
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                                                                GACACTCGAGCTGCCCCGCGACCTGGGCCGAGCTGCCTACAACCTGGGCCCAGGTGCCTG
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Pred. No. 0;
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1334 CCCGOCCCCGAGGGCCTTTCTCACCTTTCTCACTGCTCTAATTGTGTGCAT 127953 1334 CCCGGCCCCCGAGGGCCTTTCTCACCAGCACCTTCTCACTGCTCTAATTGTGTGCATT 127953 1334 CCCGGCCCACCGGCCCCCCGGCCCCCGGCCCCGGCCCCCGGCCCCCC	RESUI AC009	Db dd	D Qy	Db Qy	Qy db	Db Db	Qу Дъ	Qγ Db	Qy Db	Qy Db	Db Qy	Qy db	Qy db	Qу	Qy db	90 VQ	, da	g 99	Db
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n,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
P., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,
R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
as,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,
is,N., McLaughlin,J.,
im,J., Molla,M., Morris,M., Morrow,J., Mychalecky,J.,
r,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
son,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
son,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
ye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
e.T.J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
      12440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site: http://www-seq.wi.mit.edu
act: sequence submissions@genome.wi.mit.edu
----- Project Information
project name: L2099
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 185834)
, Linton,L., Nusbaum,C. and Lander,E.
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---- Genome Center
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1461: gap of 100 bp
3202: contig of 1741 bp in length
3302: gap of 100 bp
4619: contig of 1317 bp in length
4719: gap of 100 bp
5821: contig of 1102 bp in length
5921: gap of 100 bp
6419: contig of 498 bp in length
6519: gap of 100 bp
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8242: contig of 1723 bp in length
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Db	1933 CGCGACTGAGGCCCGGGAGGCGGGGGGGGGGGGGGGGGG	, p. 69
δ B 7	1873 CTGGGAGCGGGTGGCGGCGGCCGGCCCGGGCCCGGGCGGTGATTGGCCGCCTGCTGGC 1932	Db 99
Q B !	1813 CCCCGCACTCGCCTACCCGGCCCCGGGCGGCGGCGGCCCATGCGGCTGGGGGGGG	dg VQ
O B 1	1754 CCATCGATCCGGGAGGCCGCGGGTTCCCTTGCTTTGCCGCCGGGAGCGGCGCACGC-AG 1812	95 97
O B	1694 CCTGCCCCGGCAGGGGGATGTGGCGATGGGTGAGGGTCATGGGGTGTGAGCATCCCTGAG 1753	g V
Best Matcl	1634 CCGAGGTGGAACTATGGCAACGGGCGACCAATCAGAAGGCGCGTTGTTGCCGCGGAAGCCC 1693 	g 99
ORIG	1574 CAGGTAGCTGTACTGCAACTGTCGGCCCAAACCAATCAAGAGACGTGTTATTGCCG 1633 	Db Q
FEATUR	1514 CGCAGCCGGCCCAGCTGGGGAGCATGCGCAGTGGCCGGAGCCGGGTTGCCCGCGCCACAG 1573	D Q
AUTHO TITLI JOURI	1454 TCCGGCCAGCACCCACCTTCACCCAGTTCCGTCAGTCGCCACCTCCCTTCCCGCGTC 1513	B 8
REFE OF	1394 AAACCTGACCGCGCGCACGTCCGGGCCCGAGGGAGCAGAACAAGAGGCACCCGGACCCTCC 1453	B 84
ACCESSI VERSION KEYWORI	1334 CCCGGCGCCCAGGGGCTTGTGAGCAGCAGGTGCGCGTTCCAGGCAGCTCCAGCGACCCTT 1393	8 8
RESU AX14 LOCU	1274 CAAGAATTAGACCTCCGATAACGTTAACACCCACTTTCTCACTGCTCTAATTGTGTGCAT 1333	8d 8d
Db !	1214 GACACTCGAGCTGCCCCGCGACCTGGGCCGAGCTGCCTACAACCTGGGCCCAGGTGCCTG 1273	B 8
O B 1	1154 TCAGAGCGGAGGCTGAGGAGGCGGCGTCCCCTTGCAAAGGACTGGCAGTGAGCAGATGGG 1213	D 99
6 월 1	1094 CGGACCCTAATTCTGAAACACCCTGGTAGCGAGAGACGGGCAGGAGGGGGCTGCTGCGCAC 1153	DB 29
O B 1	1034 ATTGTTCTTCAGCTATGCATAAACATGTAATTATCATCATTACTGTGATGGGGAAAAACA 1093 	Db 49
O B 1	974 AATGAAGCAAGAGTGAATTCTGAAAAGGTCTAATAAACAGTATGGAAATATCCTTGTGGG 1033 	B 8
O B	914 GAAAAAACGAGGCTCCTTATTAAAAAAAATCAGAAACAAGTCCAACAGACTCTGAGGA 973 	용양
 Q	104812 GCTACAAAAGTATGCTTTTTATGGATTACACATGTGCACGCAACTACTTTAATTACTACA 104753	ф

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                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                    Matches 483;
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Homo sapiens lysophosphatidic acid acyltransferase-epsilon
(LDAAT-e) mRNA, complete cds.
AF375789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-MAY-2001) Mol. Elliott Ave., W., Suite 400, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and expression Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF375789.1 GI:14161584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leung, D.W
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                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                        /product="lysophosphatidic acid acyltransferase-epsilon" /protein_id="AAKS4809.1" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14161585" /db_xref="GI:14180" /db_xref="GI:1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="1-acylglycerol-3-phosphate O-acyltransferase"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="LPAAT-e"
/EC_number="2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="LPAAT-e"
275. .1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="8"
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                                                                                                                                                                                          18.6%;
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                                                                                                                                                            Score 433; DB 9; 1
Pred. No. 4.3e-235;
0; Mismatches 1;
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e, WA 98119, USA
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KEYWORDS
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LOCUS
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                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                             Strauberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Schamen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsteh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheet, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.B.,

Generation and mouse CNMA semence
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Homo sapiens acid acyltransferase-epsilon,
MGC:15506 IMAGE:4129973), complete cds.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                   2 (bases 1 t
Strausberg, R.
                                                                                                                                                                                          human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
NiH-MGC Project URL: http://mgc.nci.nih.gov
NiH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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     GGGGGCGGAGGCTGGGGGGGGGGGCGGCGGCCCGGGCCCGGGCCCGGGCGGTGATTGGC
                                                                                                               GGCGCACGCACCCCCACTCGCCTACCCGGCCCCGGCGGCGGCGGCGCCATGCGGCT
                                                                                                                                                                                                                                                                                         Conservative
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DAGTPMYLVIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATHYAFDCHM
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MRRWLHERFEIKDKMLIEFYESPDPERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAG
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PlsC; Region: Phosphate acyltransferases"
/db_xref="CDD:smart00563"
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clone="MGC:19506 IMAGE:4129973"
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                                                                                                                                                                                                                                                                                                                 Score 424; DB 9;
Pred. No. 6e-230;
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                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                              Length 1503;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PN JP 2002516657-A/104

PD 11-JUN-2002

PP 22-DEC-1998 JP 2000525562

PF 22-DEC-1999 US 208/996306,09-SEP-1998 US 60/099658 PI

DANIEL COHEN, WARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC

C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC

C12N1/19,
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Prostatic cancer gene
Patent: JP 2002516657-A 104 11-JUN-2002;
GENSET
OS Homo sapiens (human)
PN JP 2002516657-A/104
PD 11-JUN-2002
PF 22-DEC-1997 US 08/996106.09-CPD-1000 TO 70/70-
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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misc feature 235. .237
polyA signal 4531. .4536.
Location/Qualifiers
                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Score 217; DB 6; L
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Best Local Similarity
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PN JP 2002516657-A/86
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PF 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN, MARTA BLUMENHFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
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PC C12NS/00,C12N15/00
CC Prostatic cancer gene
FH Key Location/Qualifiers
FT source 1.216
FT source 1.216
FT forms sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: JP 2002516657-A 86 11-JUN-2002; GENSET
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
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JP 2002516657-A/86.
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BD196497
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                                                                                                                                          CTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCGTCGTGCTC
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                     CTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTGTACTGCGTCTACCAGAGCATG
                                                                            CTGGGCACGGCGCCCACCTACGTGTTGGCCTGGGGGGTCTGGCGGCTGCTCTCCGCCTTC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 3e-111;
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Search completed: May 26, 2004, 10:29:32 Job time: 8839.79 secs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 4682)

RS Cohen, D., Blumenfeld,M., Chumakov;I. and Bougueleret,L.

Prostatic cancer gene
AL Patent: JP 2002516657-A 103 11-JUN-2002;

Brostatic cancer gene
AL GENSET

OS Homo sapiens (human)

PN JP 2002516657-A/103

PN P 22-DEC-1998 UP 200052562

PF 22-DEC-1998 UP 200052562

PF 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD, ILVA CHUMAKOV,LYDIE BOUGUELERET PC

C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC

C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC

C12N15/09,C12N15/00,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC

C12N15/00,C12N5/00,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC

C12N15/00,C12N5/00,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C
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                                                                                                                             181 GIGCICTICTICGAGAATTACACCGGGGTCCAG 216
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JP 2002516657-A/103.
Homo sapiens (human)
Homo sapiens
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BD196514
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polyA_signal 4655. ...
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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	COMMENT	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	RESULT 1 BX332287	
Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5026.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODCO10CE04QPl&cluster=5026.f. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600	Contact: Genoscope	Full-length cDNA libraries and normalization	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	1 (bases 1 to 1201)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Riikaryota: Metazoa: Chordata: Craniata: Vertehrata: Riiteleostomi:	Homo sapiens (human)	EST.	BX332287.1 GI:30337119	BX332287	cDNA clone CS0DC010YJ07 5-PRIME, mRNA sequence.	BX332287 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens	BX332287 1201 bp mRNA linear EST 02-MAY-2003		

Result No.

Score

Query Ouery DB ID a Match Length DB ID 1201 13 BX

SUMMARIES

418 369 335

19.6 18.0 15.9 14.4

13 BX332287 12 BI197695 9 AL560635 12 BI913991

BX332287 BX332287 BI197695 602757619 AL560635 AL560635 BI913991 603180569

Description

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 822)
1 (bases 1 to 822)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Faraday Avenue Genoscope sequence ID : CSODCO10CE04QP1.
Location/Qualifiers
                                                                                                                                                                               mRNA
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602757619F1 NIH_MGC_19 Homo
                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODC010YJ07"
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Pred. No. 2.6e-207;
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Homo sapiens cI
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Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM1774 row: f column: 05
High quality sequence stop: 753.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NHIMGC_19"
/clone_lib="NHIMGC_19"
/clone_lib="NHIMGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: fockI; cDNA made by oligo-dT prinning. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:4892932"
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|mol_type="mRNA"
                                                              1005 bp mRNA linear EST 31-MAY-2003 o sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED CDNA clone CSODL003YD01 5-PRIME, mRNA sequence.
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Pred. No. 1.7e-189;
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Matches 5
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1 (bases 1 to 1005)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12907288.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5026.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIo3CBO1QP1&cluster=5026.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIO03CB01QP1.
Location/Qualifiers
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                                                                                                                                                                                           CGGCTGCTCCTCCGCCCTTCCTGCCCCGCCTTCTACCAAGCGCTTGGACGACCGGCTGTAC 2162
                                                                                                                                                                                                                                                                               CTGCCCAGCGTCGTGCTCCTGGGCACGGCGCCCACCTACGTGTTGGCCTGGGGGGGTCTGG 2102
                                                                                                                                                                                                                                                                                                                                                                CGCCGAGCTGAGAAGATGCTGCTGTTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTG 2042
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                                                                                                                           TGCGTCTACCAGAGCATGGTGCTCTTCTTCGAGAATTACACCGGGGTCCAGGTGAGC 2222
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                                       CGCCTCCCGCTCCCGGGTCTCGGCGTCCACCCGAGCTCCCGGGGGGCGCGGACCTCTCCGC 2282
                                                                                                                                                                   CGGCTGCTCTCCGCCTTCCTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTCTAC
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/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
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/db_xref="taxon:9606"
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Pred. No. 6.4e-166;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11617 row: i column: 18
High quality sequence stop: 700.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                              ACCAGAGCATGGTGCTCTTCTTCGAGAATTACACCGGGGTCCAGGTGAGCCGCCTCC 2229
                                                                                                                                                                                                                                                                                              CTGAGAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCCTACCTGCCCCA
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                                                                                                                                       sequence.
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                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Torgan: brain; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EOORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                                              (Invitrogen). Research Genethis is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7-3.5 kb. Library is full-length clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:5244761"
/lab_host="DH10B"
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                           14.4%; but
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                   Score 335; DB 12; 1
Pred. No. 1.5e-149;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library is normalized and enriched for clones and was constructed by C. Gruber Research Genetics tracking code 017. Note:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602866369F1 NIH_MGC_7 Homo
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Contact: Robert Strausberg, Ph.D.
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BI116158.1
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Tissue Procurement: DCTD/DTP
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                              GCGGCCCGGGCCCGGGCGGTGATTGGCCGCCTGCCTGCCGCACTGAGGCCCCGGGAGGCG
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                                                                                       CGGGCGGCGGCGGCCCATGCGGCTGGGGGCCGAGGCTGGGAGCGGGTGGC-GGGCGCG
                                                                                                                              GGTTCCCTTGCTTTGCCGCCGGGAGCGGCACGCAGCCCCGCACTCGCCTACCCGGCCC
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                                                                      CGGGCGGCGCCCATGCGGCTGGGGGCGGAGGCTGGGAGCGGGTGGCTGGGCGCG
            GCGGCCCGGGCCCGGTGATTGGCCGCCTGCTGGCCGACTGAGGCCCGGGAGGCC
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.8e-147;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML807 row: o column: 17
High quality sequence stop: 681.
Location/Qualifiers
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602752872F1 NIH_MGC_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGAATTACACCGGGGTCCAG 502
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                                                                                                                   /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                        /tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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                       12.5%;
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Score 291; DB 12;
Pred. No. 2.3e-128;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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www-bio.llnl.gov/bbrp/image/image.html
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                             0-233, >GC_rich#Low_complexity
primer: M13 Forward
                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGB:3066752"
/tissue_type="Jymph"
/cell_type="garminal center B 
/lab_host="DH10B (LTI)"
/clone lib="MIH_MGC_50"
/clone="Vector: pT7T3-Pac; Site 1: Not1; Site 2: Eco RI;
/note="Vector: pT7T3-Pac; Site 1: Not1; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
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Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW969608 644 bp mRN EST381685 MAGE resequences, MAGK Homo AW969608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                                                                               ATATATATATATATATATATATATATATATATGGTAAAGCATTCGGCATTCTTTTAAAGT
                                                                                                         ATATATATATATATATATATATATATATATATATGGTAAAGCATTCGGCATTCTTTAAAGT 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute for Genomic Research
Medical Center Dr., Rockville,
301 838 3528
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                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             johnq@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone_lib="MAGE resequences,
/note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"

mol_type="mRNA"
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99.7%;
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3GCC 1922 	1863 GGGGCGGAGGCTGGGAGCGGGTGGCGGCCGGGCCCGGGCCCGGGCGCGGGTGATTGGCC	- <u>,</u> 8
3CTG 1862 3CTG 232	1803 GCGCACGCAGCCCGCACTCGCCTACCCCGGCCCCGGGCGGCGCGCCCATGCGGCTG	Qy Db
Gaps 0;	y Match 11.2%; Score 261; DB 9; Length 1201; Local Similarity 99.3%; Pred. No. 6.1e-114; hes 411; Conservative 0; Mismatches 3; Indels 0;	Query M Best Lo Matches
rimed ched, oned into	/organism="Homo sapien /mol_type="mRNA" /db xref="taxon:9606" /clone="CSODA011YG14" /tissue type="NSUROBLA /clone_Iib="Homo sapie /note="Vector: pCMVSPO with a NotI-oligo(dT) double-strand cDNA was the Not I and EcoRV si Library was not normal	ORIGIN
fr oof 26.f For Contact :	Genoscope - Centre National de Sequencage BP 191 91006 EWRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns. Library was constructed by Life Technologies, a division Invitrogen. This sequence belongs to sequence cluster 50 more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODA011BD07QP1&cluster=5026.f. Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation Faraday Avenue Genoscope sequence ID: CSODA011BD07QP1. Location/Qualifiers rce	FEATURES
	AT. RS	REFERENCE AUTHORS TITLE JOURNAL COMMENT
MAY-2003	AL518744 Homo sapiens NEUROBLASTOMA HOMO sapiens CDN CSODAOLIYG14 5-PRIME, mRNA sequence. AL518744 AL518744 AL518744.2 GI:30537349 EST EST Homo sapiens (human) M Homo sapiens	RESULT 9 AL518744 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
•	958 CAACAGACTCTGAGGAAATGAAGCAAGAGTGA 989 	ОУ
AGTC 957 AGTC 205	898 TACTTTAATTACTACAGAAAAAAAGGAGGCTCCTTATTAAAAAAAA	D Q
7AAC 897 7AAC 265	838 GTAGCTTTTAGTGAAGGCTACAAAAGTATGCTTTTTATGGATTACACATGTGCACGCAAC 	Db Qy
TTC 837	778 GAAAGATCCAAAAGTCCTGTGGATCTGCTTTAACATCAATAAAACAGTTATCCACCCTTC	Qy Qy
AGGA 385	444 ACAACTATCCTTGAAAAGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGAAGG	Db .

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JOURNAL COMMENT
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AUTHORS
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BE247552
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340 bp mRNA linear EST 03-OCT-20
TCBAP2E4537 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4537, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: clones@txccc.ord
Citation: Carninci,P. and Hayashizaki,Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 340)

Wei,Y., Teang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.

Pediatric Leukemia cDNA Sequencing Project
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Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGAGCTGAGAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTG 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGTCTACCAGAGCATGGTGCTCTTCTTCTTCGAGAATTACACCGGGGTCCAG 2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCCAGCGTGCTGCTCGTGGGCACGGCGCCCACCTACGTGTTGGCCTGGGGGGGTCTGG 2102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTGCTGGCCGACTGAGGCCCGGGAGGSGGCGGGGAGCGCAAGCTCGCTGC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGCTGGCCGCGACTGAGGCCCGGGAGCGGGGGGGGAGCGCAGGCGGAGCTCGCTGC 1982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832-825-4038
/Glone lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA" [note="Vector: lambda pSB; Site 1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCGCAGGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGGATCGGATCGGACTCGCATCCGCATCCGCACTCGCATTCGTATAT(C) 3']
Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP4537"
                                                                                                                                                                                                                                                          /tissue_type="leukopheresis"
/call_type="per-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:9099309
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BX473402
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247;
                                                                                                                                                                                                                           Please contact the RZPD: Ressourcenzent
Berlin- Charlottenburg, GERMANY; Email:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S. EST (Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX473402 567 bp mRNA linear DKFZp686F16162_r1 686 (synonym: hlcc3) Homo sapiens DKFZp686F16162_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                 sequenced by MediGenomix (Martinsried/Germany) within the sequencing consortium of the German Genome Project. No s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX473402.1 GI:31667652
                                                                                                                                                                                                                                                                                                   This clone (DKFZp686F16162) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTAATAAACAGTATGGAAATATCCTTGTGGGATTGTTCTTCAGCTATGCATAAACATG 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACACATGTGCACGCAACTACTTTAATTACTACAGAAAAAAACGAGGCTCCTTATTAAAAA 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAATCAGAAACAAGTCCAACAGACTCTGAGGAAATGAAGCAAGAGTGAATTCTGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAATTATCATCATTACTGTGATGGGGAAAAACACGGACCCTAATTCTGAAACACCCTGGT
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/clone="DKFZp686F16162"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="486 (synonym: h
/note="Vector: pTriplEx2; S
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                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.5e-107;
                                                                                                                                                                                                                                                  Ressourcenzentrum, Heubnerweg GERMANY; Email: clone@rzpd.de.
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hlcc3)"
Site_1: SfiIA;
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REFERENCE
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COMMENT
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BU154303
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Best Local Similarity
Matches 227; Conserv
                                                                  Matches
                                                                                Query Match
Best Local
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
Unpublished (1999)
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AGENCOURT_7832759 NIH_MGC_
                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 242.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13469 row: j column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
BU154303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU154303.1
                                                                                    Similarity
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                                  GTCATGGGGTGTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCCTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTCCGCCTTCCTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTGTACTGCGTCT 2169
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens (human)
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                                                                                                                                                    /tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 67"
/note="Corgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6144491"
                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:22667835
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100.0%; Pr
                                                                                  9.8%;
                                                                                  Score 227; DB 13; pred. No. 1.4e-97;
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Pred. No.
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3_67
                                                                    Mismatches
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Homo
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1 (bases 1 to 687)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM789163 687 bp mRNA linear EST 05-MAR-2002 K-EST0068703 S11SNU1 Homo sapiens cDNA clone S11SNU1-25-E07 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 687.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: yongsung@mail.kribb.re.kr
Plate: 25 row: E column: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21C Frontier Korean EST Project 2001
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9.6%;
ilarity 100.0%;
Conservative
                                                                                                                                                             /note="Torgan; Stomach; Vector: pME18-FL3; Site_1: XhoI; /note="Torgan; Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfil site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript I using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII digested pME188-FL3 vector. The
                                                                                          obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Lymphoblast-like"
/cell_line="SNU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="Stomach"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="S11SNU1"
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 Score 223; DB 12;
; Pred. No. 1.2e-95;
0; Mismatches 0;
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1994 GAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCGT 2053
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2949 row: m column: 12
High quality sequence stop: 269.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:6671220"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH1 MGC_109"
/clone_lib="NIH1 libe="NIH1 
                                                                                                                                                                                                                                                                                                      NIH_MGC Library."
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|mol_type="mRNA"
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9.5%; Score 221; DB 13; 100.0%; Pred. No. 1.1e-94; tive 0; Mismatches 0;
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                                                                                                                                Length 1216;
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Oy 2120 CCTGC	Qy 2060 CCTGG Db 62 CCTGG	Oy 2000 GCTGC Db 2 GCTGC	Query Match Best Local Simila Matches 217; Co	ORIGIN	German No 81 st No 81 st This cl Please the Please Serlin-German Serlin-German Serlin-German Serlin-German Serlin-German Serline Serli	Ingolsti Ingolsti This is Clone fi Research Bequency	TITLE EST (Pou Wellenre JOURNAL Unpublis COMMENT Contact:	REFERENCE 1 (bases AUTHORS Poustka, A. Wiemann S. Wiemann S.	ACCESSION BX507409 VERSION BX507409.1 KEYWORDS EST. SOURCE Homo sapier ORGANISM Homo sapier	RESULT 15 BX507409 LOCUS DEFINITION DEFENTION DEFENTION DEFENTAGE	Qy 1919 GGCGG Db 214 GGCGG	Qy 1859 GCTGG Db 154 GCTGG	Db 94 AGCGG
CCTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTGTACTGCGTCTACCAGAGCAT 2179	CCTGGGCACGGCGCCCACCTACGTGTTGGCCTGGGGGGGTTCTGGCGGCTGCTCTCCGCCTT 2119	GCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCGTCGTGCT 2059	h 9.3%; Score 217; DB 13; Length 643; Similarity 100.0%; Pred. No. 9.4e-93; 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	" :9606" 90084" 11" 11" (synonym pSport1_S	Berlin. 6, 1405	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@kkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the	ustka,A., Albert,R., Moosmayer,P., Schupp,I., euther,R., et al.) shed (2003) : MIPS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 643) Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann S.	GI:32051430 is (human)	9 90084 r1 779 (synonym: hncc1) Homo sapiens cDNA clone 90084 r, mRNA semience.	GGCCGCTGCTGGCCGCGACTGAGGCCCGGGAGGCGGGCGG	GCTGGGGGGGAGGCTGGGAGCGGGTGGCGGGCGCGGGCCCGGGCCCGGGCGGG	

Search completed: May 26, 2004, 12:51:02 Job time : 5471.68 secs

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AUTHORS
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asteride; campanulide; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 209)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
Intpil/compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                            BQ989814
QGF18L11.yg.abl QG_EFGHJ
QGF18L11, mRNA sequence.
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Copartment of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
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AL223828 Tetraodon
AL213828 Tetraodon
AV334716 AV334716
AZ726944 RPCI-24-1
BQ597016 PFESTOAD2
AI431315 ar55b09.x
BH742910 gz67b11.g
AI063012 GH02422.5
BH459006 BOHGB16TF
CE279192 tigr-gss-
CA993731 pAR10A02
AG144022 Pan trog1
BZ50828 BONHJ80TF
BZ5070860 lki79e10.
AK013575 Mus muscu
AK013575 Mus muscu
AV254417 AV254417
AI032180 or96a11.s
B1288613 UI-R-DK0-
BB24365 BB244365
AI435529 th73e07.x
BZ88941 CH240_232
AW44852 UI-R-BU09
BQ492779 EST01945
BM106873 510932 MA
CE610771 tigr-gss-
CC557326 CH240_256
BX721433 BX721433
BZ885349 CFESTOGA1
BG5251596 NISC n111
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BI586329 RH26255.5
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BU013709 QGJ5G07.y
BQ091419 QGE13L15.
AV665533 AV665533
BU011575 QGJ16J71.
AV665534 AV665534
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EST 21-AUG-2002

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RESULT 2
BQ847561
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QGA3g09, mRNA sequence.
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y..
Lai,Z., Church,S., Jackson,L. and Bradford,K.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; Asteraceae; Cichorioideae;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
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Plate: QGF18
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                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                        http://compgenomics.ucdavis.edu/
Unpublished (2002)
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Fax: 1-(530)-752-9659
                                                                                                                                      Email: akozik@atgc.org (michelmore@vegmail.ucdavis.edu)
belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=GTTGCACGGG"
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
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(mol_type="mRNA"
/cultivar="L.serriola"
                    organism="Lactuca sativa"
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type="mRNA"
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KEYWORDS
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1 (bases 1 to 210)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project Lettuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; campanulids; Asterales; Asteraceae; Cichorioideae;
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23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Asmundson Hall, UCD, 1
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                        Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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te: QGB9 row: A
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/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
/clome_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
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TAG_LIB=QG_ABCDI lettuce salinas
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/clone="QGA3g09"
/lab_host="E.coli"
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/clone="QGB9A22"
                                                                                                                        /lab_host="E.coli"
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|mol_type="mRNA"
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100.0%; Pr
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REFERENCE
AUTHORS
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1 (bases 1 to 222)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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Unpublished (2002)
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Lactuca sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     details.
te: QGF25
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                                                                                                                 Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
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                  TAG_TISSUE=roots
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=GTTGCACGGG"
                                                                                         construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                 /clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:4236"
clone="QGF25I03"
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cultivar="L.serriola"
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Pred. No.
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RESULT 5
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Best Local S
Matches 23
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Contact: Alexander Kozik [R.W.Michelmore]
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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1 (bases 1 to 223)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Leituce and Sunflower ESTs from the Compositae Genome Project
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Plate: QGA2
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belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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                                                                                                                                                                                                                                                                  /clone lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                                    TAG_TISSUE=roots
TAG_LIB=QG_ABCDI lettuce salinas
TAG_SEQ=GTTGCACGGG"
                                                                                                                                                                                                                                                 construction can be obtained at http://cgpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4236"
/clone="QGA2a06"
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/cultivar="Salinas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'lab_host="E.coli"
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100.0%; Pr
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k; Pred. No. 23;
0; Mismatches
                                                                                score 23; DB; Pred. No. 23; 0; Mismatches
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23;
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RESULT 7
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                BQ981419
353 bp mRNA linear EST 21-AUG-2002 QSE13L15.yg.abl QG EFGHJ lettuce serriola Lactuca sativa cDNA clone QGE13L15, mRNA sequence.
BQ981419
BQ981419 GI:22398942
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Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
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Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nttp://compgenomics.ucdavis.edu,
Unpublished (2002)
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QGJ5G07.yg.ab1 QG_EFGHJ lettuce
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belongs to contig QG_CA_Contig7771, see http://cgpdb.ucdavis.edu/
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Fax: 1-(530)-752-9659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGJ5G07, mRNA sequence.
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TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=GTTGCACGGG"
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construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype
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/db_xref="taxon:4236"
/clone="QGJ5G07"
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k; Pred. No. 22;
0; Mismatches
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AUTHORS
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KEYWORDS
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                              AV665533 Bos taurus brain
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
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Establishment of a high throughput EST sequencing system using
                              and Sugimoto,Y.
                                                 1 (bases 1 to 432)
Takasuga, A., Hirotsune, S., Itoh, R.,
                                                                                                                                                                                     Bos taurus
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                                                                                                                                                                                                                                                                    AV665533.1
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AV665533
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belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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Unpublished (2002)
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TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=CGĀATGCGGG"
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
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Location/Qualifiers
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Pred. No.
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BU011575 ------ QGJ16J21.yg.abl QG_BFGHJ lettuce serriola Lactuca sativa cDNA clone QGJ16J21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                             Contect: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                Cichorieae; Lactuca.

1 (Dases 1 to 551)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing.
This clone was obtained from a polyA-deleted
Location/Qualifiers
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
21570554
11713328
                                                                                                                                                                                                                                                                                                http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                          Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
                                                                                                                                                                        Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU011575.1 GI:22445970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactuca sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                     details.
:e: QGJ16 row: J
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Conservative
                                                               Location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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(tissue_type="brain"
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lab_host="DH10B"
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Pred. No.
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                                                                                                                            see http://cgpdb.ucdavis.edu/
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                           Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                                                                                                                                                                                        Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshikazu Sugimoto
Animal Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poly(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takasuga, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                      le pass sequencing.
                                                                                                                                                                                                                                   clone was obtained from a
                                                                                                                                                                                                                                                                                              81-248-25-5725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ishment of a high throughput EST sequencing syst
) tail-removed cDNA libraries and determination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_TISSUE=flowers pre-fertilized
TAG_LIB=QG_EFGHJ_lettuce serriola
was deleted from a Not1 site"
            /clone="ElBR049B04"
/tlssue_type="brain"
/dev_stage="fetus"
/lab host="DH108"
/lab host="Bos taurus brain fetus"
/clone_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                          organism="Bos taurus"
                                                                                                                                                                                                               location/Qualifiers
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/clone="QGJ16J21"
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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GSS; genome survey sequence.
Tetracdon nigroviridis
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
203123 of library G from Tetraodon nigroviridis, genomic survey
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23; Conserv
                                                                                                                                                                                                                                                                                                                                 scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
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20296633
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                                              TCTTTTTTCTTGAATTGTTTTT 523
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llarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                    clone_lib="G"
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                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis'
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                      note="Genoscope sequence ID : COAG203AE12SP1~end"
                                                                                                                                                                                                                                                      db_xref="taxon:99883"
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17;
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166C04 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-APR-2000) Genoscope - Centre National de Sequencage: Bp 191 91006 EVRY cedex - FRANCE (B-mail: seqrefægenoscope.cns.fr - Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                  AV334716 236 bp mRNA linear EST AV334716 RIKEN full-length enriched, adult male medulla Mus musculus cDNA clone 6330563N19 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Mus musculus
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Direct Submission
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Tetraodon nigroviridis
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA
/db_xref="taxon:99883"
/clone="166C04"
                                                                                                                                                                                                                                                                                                                                                                          note="Genoscope sequence"
                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="G"
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Pred. No.
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Mus musculus

Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus musculus (house mouse)

GI:6374768

AV334716.1 EST.

24-JAN-2001

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
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                        Similarity
2.0%; Solitarity 100.0%; If Conservative 0;
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                                                                                                                               /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                 from Lambda
BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="medulla oblongata"
/dev_stage="adult"
/dev_stage="pH10B"
/clone_lib="RIKEN full-length enriched, adult male medulla
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PESTOab25f02.yl Plasmodium falciparum 3D7
Falciparum 3D7 cDNA 5', mRNA sequence.
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AZ726944
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Seq primer: T7
Class: BAC ends.
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AZ726944.1 GI:12475337
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BQ597016.1
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegnye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTTTAAAATAAAATTTTTT 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATTTTAAAATAAAATTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 to 367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RPCI-24-113I24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism≃"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:10090"
                          GI:21543742
                                                                                                                                                                                                                                                                                                                                                2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _type="Spleen/Brain"
e_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                Score 22;
; Pred. No.
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                   58
8
                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                      Length 367
                                                                                             linear EST 24-JUN-2002 asexual cDNA Plasmodium
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Search completed: May 26, 2004, 12:51:08 Job time : 2588.32 secs
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                         127 TTTAAAATAAATTTTTTTAA 148
                                                                                                                                                                                                         510 TITAAAATAAAATTTTTTTAA 531
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Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 423.
Location/Qualifiers
                                                                                                                                                                                                                                                                            2.0%; Score 22; DB 13; Length 424; ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ub Asel="caxon:30329"
/lab host="Diagnodium falciparum 3D7 asexual cDNA"
/clone lib="Plasmodium falciparum 3D7 asexual cDNA"
/clone lib="Plasmodium falciparum 3D7 asexual cDNA"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
expthrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Promega, WI) using streptavidin
Magnesphere particles. Directional CDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and KNoI sites of 1 ZapII vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the ExAssist helper phage
(Stratagene), the phagemids were precitptated with PEG
8000 and extracted with phenol/chloroform. Phagemid DNA
was electroporated into DH10B cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Plasmodium falciparum 3D7"
/mol_type="mRNA"
/db xref="taxon:36329"
/lab_host="DH10B (GeneHog. Truitronn)
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                       0;
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